



ENTERED

PCT10

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/048,116

DATE: 07/17/2002
 TIME: 09:33:37

Input Set : A:\EP.txt
 Output Set: N:\CRF3\07172002\J048116.raw

3 <110> APPLICANT: C.N.R.S.
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED FROM
 THESE PROTEINS,
 6 ANALOGOUS TO MOLECULES INVOLVED IN IMMUNE RESPONSES
 8 <130> FILE REFERENCE: CP/BB 1181
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/048,116
 C--> 11 <141> CURRENT FILING DATE: 2002-05-24
 13 <160> NUMBER OF SEQ ID NOS: 2
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1484
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial sequence
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(1482)
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Description of Artificial Sequence: ligation
 28 fragments of DNA
 30 <400> SEQUENCE: 1
 31 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc 48
 32 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
 33 1 5 10 15
 35 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta. 96
 36 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
 37 20 25 30
 39 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag 144
 40 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
 41 35 40 45
 43 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat 192
 44 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
 45 50 55 60
 47 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc 240
 48 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
 49 65 70 75 80
 51 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac 288
 52 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
 53 85 90 95
 55 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag 336
 56 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
 57 100 105 110
 59 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag 384
 60 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
 61 115 120 125

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63	ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc	432
64	Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile	
65	130 135 140	
67	aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat	480
68	Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr	
69	145 150 155 160	
71	gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct	528
72	Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser	
73	165 170 175	
75	tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg	576
76	Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val	
77	180 185 190	
79	gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag	624
80	Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu	
81	195 200 205	
83	att cca gcc ccc atg tca gag ctg aca gaa act gga ggt gga gga tcc	672
84	Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser	
85	210 215 220	
87	act aca gct cca tca gct cag ctc gaa aaa gag ctc cag gcc ctg gag	720
88	Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu	
89	225 230 235 240	
91	aag gaa aat gca cag ctg gaa tgg gag ttg caa gca ctg gaa aag gaa	768
92	Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu	
93	245 250 255	
95	ctg gct cag gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt	816
96	Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys	
97	260 265 270	
99	cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc	864
100	Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val	
101	275 280 285	
103	ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc	912
104	Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser	
105	290 295 300	
107	ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat	960
108	Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp	
109	305 310 315 320	
111	gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag	1008
112	Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln	
113	325 330 335	
115	aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt	1056
116	Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser	
117	340 345 350	
119	gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa	1104
120	Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys	
121	355 360 365	
123	tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc	1152
124	Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile	
125	370 375 380	
127	tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct	1200

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128 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
129 385                               390                               395                               400
131 cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg 1248
132 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
133                               405                               410                               415
135 gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac 1296
136 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
137                               420                               425                               430
139 ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct 1344
140 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
141                               435                               440                               445
143 gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac 1392
144 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
145                               450                               455                               460
147 tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg 1440
148 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
149 465                               470                               475                               480
151 cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aa 1484
152 His Asn His His Thr Lys Ser Phe Ser Arg Thr Pro Gly
153                               485                               490
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 921
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of artificial sequence: Ligation
164 fragments of DNA
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(921)
170 <400> SEQUENCE: 2
171 atg gct ctg cag atc ccc agc ctc ctc ctc tca gct gct gtg gtg gtg 48
172 Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val
173 1 5 10 15
175 ctg atg gtg ctg agc agc ccc ggg act gag ggc gga aac tcc atc tgc 96
176 Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys
177 20 25 30
179 ttc tcg ccg tcg ctg gag cac ccg atc gtg gtg tcc ggc agc tgg gac 144
180 Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp
181 35 40 45
183 gga ggt ggg ggc tca cta gtg ccc cga ggc tct gga ggt gga ggc tcc 192
184 Gly Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser
185 50 55 60
187 gaa agg cat ttc gtg gtc cag ttc aag ggc gag tgc tac tac acc aac 240
188 Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn
189 65 70 75 80
191 ggg acg cag cgc ata cgg ctc gtg acc aga tac atc tac aac cgg gag 288
192 Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu
193 85 90 95

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```

195 gag tac gtg cgc tac gac agc gac gtg ggc gag tac cgc gcg gtg acc 336
196 Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
197      100      105      110
199 gag ctg ggg cgg cca gac gcc gag tac tgg aac agc cag ccg gag atc 384
200 Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile
201      115      120      125
203 ctg gag cga acg cgg gcc gag gtg gac acg gcg tgc aga cac aac tac 432
204 Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr
205      130      135      140
207 gag ggg ccg gag acc agc acc tcc ctg cgg cgg ctt gaa cag ccc aat 480
208 Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn
209 145      150      155      160
211 gtc gcc atc tcc ctg tcc agg aca gag gcc ctc aac cac cac aac act 528
212 Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr
213      165      170      175
215 ctg gtc tgt tcg gtg aca gat ttc tac cca gcc aag atc aaa gtg cgc 576
216 Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg
217      180      185      190
219 tgg ttc agg aat ggc cag gag gag aca gtg ggg gtc tca tcc aca cag 624
220 Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln
221      195      200      205
223 ctt att agg aat ggg gac tgg acc ttc cag gtc ctg gtc atg ctg gag 672
224 Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu
225      210      215      220
227 atg acc cct cat cag gga gag gtc tac acc tgc cat gtg gag cat ccc 720
228 Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro
229 225      230      235      240
231 agc ctg aag agc ccc atc act gtg gag tgg agg gca cag tcc gag tct 768
232 Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser
233      245      250      255
235 gcc cgg agc aag gga ggt gga gga tcc act aca gct cca tca gct cag 816
236 Ala Arg Ser Lys Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln
237      260      265      270
239 ttg aaa aag aaa ttg caa gca ctg aag aaa aag aac gct cag ctg aag 864
240 Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys
241      275      280      285
243 tgg aaa ctt caa gcc ctc aag aag aaa ctc gcc cag cat cat cat cat 912
244 Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln His His His His
245      290      295      300
247 cat cat tga 921
248 His His
249 305

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/048,116

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Input Set : A:\EP.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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TIME: 09:33:38

Input Set : A:\EP.txt

Output Set: N:\CRF3\07172002\J048116.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date